

Supplementary Material

Clinical Characteristics	ME/CFS	Controls
Median age	36.4	38.8
Gender	F = 6 M = 4	F = 6 M = 4
Nationality	NZ/European = 10	NZ/European = 10
Stage of illness	Acute = 8 Chronic = 1 Unsure = 1	NA
Median length of illness	12.6 years	NA
Reported trigger of illness	Vaccination = 1 Glandular Fever = 6 Stress = 1 Infection = 1 Unsure = 1	NA

Supplementary Table S1. The New Zealand ME/CFS study group.

Supplementary Table S2. The differentially expressed gene transcript ($P < 0.05$) dataset analyzed by Ingenuity Pathway Analysis.

Gene Name	Symbol	Fold Change	P-value
Interleukin 8	<i>CXCL8/IL8</i>	5.57	2.49x10 ⁻⁶
NFKB inhibitor alpha	<i>NFKBIA</i>	2.40	2.01x10 ⁻⁵
TNF alpha induced protein 3	<i>TNFAIP3</i>	3.73	1.3x10 ⁻⁴
Jun proto-oncogene, AP-1 transcription factor subunit	<i>JUN</i>	2.51	3.79x10 ⁻⁴
period circadian regulator 1	<i>PER1</i>	2.34	8.75x10 ⁻⁴
ubiquitin conjugating enzyme E2 D3	<i>UBE2D3</i>	1.98	2.2x10 ⁻³
nicotinamide phosphoribosyltransferase	<i>NAMPT</i>	1.90	2.3x10 ⁻³
RB binding protein 6, ubiquitin ligase	<i>RBBP6</i>	2.14	2.3x10 ⁻³
ankyrin repeat domain 46	<i>ANKRD46</i>	0.66	2.43x10 ⁻³
immediate early response 3	<i>IER3</i>	2.03	2.71x10 ⁻³
zinc finger CCCH-type containing 12A	<i>ZC3H12A</i>	1.76	2.78x10 ⁻³

cAMP responsive element modulator	<i>CREM</i>	1.90	2.83x10 ⁻³
receptor interacting serine/threonine kinase 2	<i>RIPK2</i>	1.57	3.28x10 ⁻³
phorbol-12-myristate-13-acetate-induced protein 1	<i>PMAIP1</i>	2.25	3.31x10 ⁻³
protein phosphatase 1 regulatory subunit 15A	<i>PPP1R15A</i>	1.69	3.64x10 ⁻³
ectodermal-neural cortex 1	<i>ENC1</i>	2.15	4.25x10 ⁻³
peptidase, mitochondrial processing beta subunit	<i>PMPCB</i>	1.87	4.27x10 ⁻³
lysophosphatidic acid receptor 1	<i>LPAR1</i>	0.57	4.28x10 ⁻³
G3BP stress granule assembly factor 2	<i>G3BP2</i>	2.01	4.48x10 ⁻³
phosphatidylinositol glycan anchor biosynthesis class A	<i>PIGA</i>	1.83	4.88x10 ⁻³
cyclin L1	<i>CCNL1</i>	1.59	5.25x10 ⁻³
suppressor of cytokine signaling 3	<i>SOCS3</i>	1.78	5.32x10 ⁻³
cysteine and serine rich nuclear protein 1	<i>CSRNPI</i>	1.58	5.65x10 ⁻³
protocadherin gamma subfamily C, 3	<i>PCDHGC3</i>	0.57	5.84x10 ⁻³
zinc finger protein 274	<i>ZNF274</i>	1.55	6.06x10 ⁻³
ubiquitin specific peptidase 3	<i>USP3</i>	1.80	6.2x10 ⁻³
zinc finger protein 202	<i>ZNF202</i>	0.55	6.8x10 ⁻³
paired immunoglobulin-like type 2 receptor beta	<i>PILRB</i>	1.46	7.26x10 ⁻³
heparan sulfate-glucosamine 3-sulfotransferase 3B1	<i>HS3ST3B1</i>	0.67	8.03x10 ⁻³
DEAD-box helicase 3, X-linked	<i>DDX3X</i>	1.51	8.23x10 ⁻³
kelch like family member 15	<i>KLHL15</i>	1.83	9.22x10 ⁻³
eukaryotic translation termination factor 1	<i>ETF1</i>	1.84	9.98x10 ⁻³
defective in cullin neddylation 1 domain containing 3	<i>DCUN1D3</i>	0.64	1.01x10 ⁻²
fat storage inducing transmembrane protein 2	<i>FITM2</i>	0.67	1.06x10 ⁻²
TWIST neighbor	<i>TWISTNB</i>	1.63	1.12x10 ⁻²
CDC like kinase 1	<i>CLK1</i>	1.68	1.15x10 ⁻²
Ras association domain family member 1	<i>RASSF1</i>	0.66	1.16x10 ⁻²
zinc finger protein 267	<i>ZNF267</i>	1.57	1.21x10 ⁻²
chromosome 1 open reading frame 74	<i>Clorf74</i>	0.62	1.25x10 ⁻²
GABA type A receptor associated protein like 1	<i>GABARAPL1</i>	1.61	1.28x10 ⁻²
tripartite motif containing 5	<i>TRIM5</i>	0.71	1.28x10 ⁻²
PHD finger protein 1	<i>PHF1</i>	1.41	1.3x10 ⁻²
capicua transcriptional repressor	<i>CIC</i>	1.45	1.31x10 ⁻²
growth arrest and DNA damage inducible beta	<i>GADD45B</i>	1.59	1.33x10 ⁻²
transformer 2 beta homolog	<i>TRA2B</i>	1.59	1.33x10 ⁻²
TCDD inducible poly(ADP-ribose) polymerase	<i>TIPARP</i>	1.83	1.42x10 ⁻²
lysophosphatidic acid receptor 5	<i>LPAR5</i>	0.66	1.43x10 ⁻²
heterogeneous nuclear ribonucleoprotein H1	<i>HNRNPH1</i>	2.48	1.46x10 ⁻²
SBDS, ribosome maturation factor	<i>SBDS</i>	1.52	1.49x10 ⁻²
U2 snRNP associated SURP domain containing	<i>U2SURP</i>	1.58	1.5x10 ⁻²
cyclin dependent kinase 16	<i>CDK16</i>	1.48	1.51x10 ⁻²
nuclear receptor subfamily 4 group A member 2	<i>NR4A2</i>	2.18	1.52x10 ⁻²
kelch repeat and BTB domain containing 2	<i>KBTBD2</i>	1.49	1.56x10 ⁻²
superoxide dismutase 2	<i>SOD2</i>	1.59	1.63x10 ⁻²

chromodomain helicase DNA binding protein 2	<i>CHD2</i>	1.93	1.64x10 ⁻²
ADP ribosylation factor like GTPase 4A	<i>ARL4A</i>	1.77	1.65x10 ⁻²
protein kinase D3	<i>PRKD3</i>	1.83	1.65x10 ⁻²
free fatty acid receptor 2	<i>FFAR2</i>	1.61	1.72x10 ⁻²
zinc finger protein 483	<i>ZNF483</i>	1.82	1.76x10 ⁻²
PNMA family member 3	<i>PNMA3</i>	2.12	1.77x10 ⁻²
ubiquitin specific peptidase 36	<i>USP36</i>	1.55	1.77x10 ⁻²
protein kinase C eta	<i>PRKCH</i>	1.62	1.79x10 ⁻²
RNA binding motif protein 39	<i>RBM39</i>	1.58	1.81x10 ⁻²
acyl-CoA synthetase long chain family member 4	<i>ACSL4</i>	1.39	1.85x10 ⁻²
ras homolog family member Q	<i>RHOQ</i>	1.50	1.85x10 ⁻²
deltex E3 ubiquitin ligase 2	<i>DTX2</i>	0.67	1.9x10 ⁻²
zinc finger and BTB domain containing 43	<i>ZBTB43</i>	2.28	1.91x10 ⁻²
matrin 3	<i>MATR3</i>	1.63	2.03x10 ⁻²
Kruppel like factor 10	<i>KLF10</i>	1.95	2.04x10 ⁻²
KRAS proto-oncogene, GTPase	<i>KRAS</i>	1.58	2.09x10 ⁻²
RELA proto-oncogene, NF- κ B subunit	<i>RELA</i>	1.45	2.15x10 ⁻²
fem-1 homolog C	<i>FEM1C</i>	1.66	2.27x10 ⁻²
family with sequence similarity 220 member A	<i>FAM220A</i>	0.68	2.29x10 ⁻²
achaete-scute family bHLH transcription factor 2	<i>ASCL2</i>	0.55	2.32x10 ⁻²
coiled-coil domain containing 186	<i>CCDC186</i>	1.47	2.33x10 ⁻²
adrenomedullin	<i>ADM</i>	2.24	2.37x10 ⁻²
GATA binding protein 2	<i>GATA2</i>	0.54	2.39x10 ⁻²
ring finger protein 4	<i>RNF4</i>	1.70	2.39x10 ⁻²
interferon related developmental regulator 1	<i>IFRD1</i>	1.69	2.49x10 ⁻²
ZFP36 ring finger protein	<i>ZFP36</i>	1.43	2.52x10 ⁻²
coiled-coil domain containing 47	<i>CCDC47</i>	1.69	2.56x10 ⁻²
TATA-box binding protein associated factor, RNA polymerase I subunit D	<i>TAF1D</i>	1.52	2.58x10 ⁻²
immunoglobulin heavy joining 6	<i>IGHJ6</i>	0.49	2.59 x10 ⁻²
POM121 transmembrane nucleoporin	<i>POM121/POM1</i>		
erythrocyte membrane protein band 4.1 like 3	<i>21C</i>	1.40	2.6x10 ⁻²
isopentenyl-diphosphate delta isomerase 1	<i>EPB41L3</i>	0.66	2.63x10 ⁻²
zinc finger C3H1-type containing	<i>IDI1</i>	1.81	2.68x10 ⁻²
CDC like kinase 3	<i>ZFC3H1</i>	1.50	2.68x10 ⁻²
cytochrome P450 family 2 subfamily R member 1	<i>CLK3</i>	1.29	2.75x10 ⁻²
arginine and serine rich coiled-coil 2	<i>CYP2R1</i>	1.55	2.77x10 ⁻²
NFKB inhibitor zeta	<i>RSRC2</i>	1.83	2.77x10 ⁻²
protein phosphatase 1 catalytic subunit beta	<i>NFKBIZ</i>	1.82	2.79x10 ⁻²
RNA guanine-7 methyltransferase	<i>PPP1CB</i>	1.52	2.81x10 ⁻²
zinc finger protein 787	<i>RNMT</i>	1.40	2.81x10 ⁻²
trinucleotide repeat containing 18	<i>ZNF787</i>	1.58	2.81x10 ⁻²
zinc finger CCHC-type containing 11	<i>TNRC18</i>	1.38	2.83x10 ⁻²
	<i>ZCCHC11</i>	1.49	2.83x10 ⁻²

suppressor of variegation 3-9 homolog 2	<i>SUV39H2</i>	1.66	2.89x10 ⁻²
CCR4-NOT transcription complex subunit 6 like	<i>CNOT6L</i>	1.48	2.91x10 ⁻²
cold inducible RNA binding protein	<i>CIRBP</i>	1.40	3.04x10 ⁻²
outer dense fiber of sperm tails 2 like	<i>ODF2L</i>	1.53	3.05x10 ⁻²
cilia and flagella associated protein 97	<i>CFAP97</i>	1.88	3.11x10 ⁻²
programmed cell death 4	<i>PDCD4</i>	1.56	3.12x10 ⁻²
casein kinase 1 epsilon	<i>CSNK1E</i>	1.34	3.14x10 ⁻²
G protein-coupled receptor 55	<i>GPR55</i>	0.67	3.23x10 ⁻²
SPT5 homolog, DSIF elongation factor subunit	<i>SUPT5H</i>	1.43	3.25x10 ⁻²
tetratricopeptide repeat domain 39C	<i>TTC39C</i>	0.66	3.28x10 ⁻²
trafficking protein particle complex 13	<i>TRAPPC13</i>	1.47	3.29x10 ⁻²
protein phosphatase 2 scaffold subunit Aalpha	<i>PPP2R1A</i>	1.49	3.4x10 ⁻²
ninjurin 1	<i>NINJ1</i>	1.50	3.44x10 ⁻²
family with sequence similarity 109 member A	<i>FAM109A</i>	0.65	3.46x10 ⁻²
histidine triad nucleotide binding protein 1	<i>HINT1</i>	1.69	3.47x10 ⁻²
general transcription factor IIH subunit 1	<i>GTF2H1</i>	0.72	3.49x10 ⁻²
hexosaminidase D	<i>HEXDC</i>	0.72	3.52x10 ⁻²
CDC42 effector protein 1	<i>CDC42EP1</i>	1.78	3.54x10 ⁻²
mitochondrial poly(A) polymerase	<i>MTPAP</i>	1.39	3.57x10 ⁻²
kelch repeat and BTB domain containing 11	<i>KBTBD11</i>	0.70	3.6x10 ⁻²
integrin subunit beta 2	<i>ITGB2</i>	0.52	3.63x10 ⁻²
interferon induced with helicase C domain 1	<i>IFIH1</i>	1.50	3.67x10 ⁻²
treacle ribosome biogenesis factor 1	<i>TCOF1</i>	1.70	3.68x10 ⁻²
zinc finger and BTB domain containing 3	<i>ZBTB3</i>	0.70	3.74x10 ⁻²
NADH:ubiquinone oxidoreductase subunit S6	<i>NDUFS6</i>	1.38	3.75x10 ⁻²
acyl-CoA dehydrogenase very long chain	<i>ACADVL</i>	0.67	3.82x10 ⁻²
zinc finger and BTB domain containing 21	<i>ZBTB21</i>	1.99	3.86x10 ⁻²
GIPC PDZ domain containing family member 1	<i>GIPC1</i>	0.70	3.87x10 ⁻²
B cell CLL/lymphoma 6	<i>BCL6</i>	1.58	3.93x10 ⁻²
nuclear cap binding protein subunit 2	<i>NCBP2</i>	1.66	4.08x10 ⁻²
chromosome 14 open reading frame 93	<i>C14orf93</i>	1.46	4.14x10 ⁻²
ring finger protein 19A, RBR E3 ubiquitin protein ligase	<i>RNF19A</i>	1.59	4.16x10 ⁻²
splicing regulatory glutamic acid and lysine rich protein 1	<i>SREK1</i>	1.53	4.17x10 ⁻²
zinc finger protein 805	<i>ZNF805</i>	1.57	4.21x10 ⁻²
WD repeat domain 43	<i>WDR43</i>	1.87	4.24x10 ⁻²
DNA damage inducible transcript 3	<i>DDIT3</i>	1.62	4.28x10 ⁻²
zinc finger protein 292	<i>ZNF292</i>	1.38	4.31x10 ⁻²
heterogeneous nuclear ribonucleoprotein A2/B1	<i>HNRNPA2B1</i>	1.44	4.32x10 ⁻²
transformer 2 alpha homolog	<i>TRA2A</i>	1.43	4.33x10 ⁻²
nuclear factor, interleukin 3 regulated	<i>NFIL3</i>	1.72	4.41x10 ⁻²
syntaxin 5	<i>STX5</i>	1.39	4.46x10 ⁻²
zinc finger CCCH-type containing 10	<i>ZC3H10</i>	0.79	4.46x10 ⁻²
CD69 molecule	<i>CD69</i>	1.43	4.47x10 ⁻²

solute carrier family 9 member A1	<i>SLC9A1</i>	1.49	4.48x10 ⁻²
zinc finger protein 395	<i>ZNF395</i>	1.31	4.48x10 ⁻²
solute carrier family 19 member 1	<i>SLC19A1</i>	0.68	4.49x10 ⁻²
apical junction component 1 homolog	<i>AJM1</i>	0.65	4.5x10 ⁻²
coiled-coil serine rich protein 2	<i>CCSER2</i>	1.38	4.51x10 ⁻²
Tax1 binding protein 1	<i>TAX1BP1</i>	1.34	4.56x10 ⁻²
family with sequence similarity 91 member A1	<i>FAM91A1</i>	1.58	4.64x10 ⁻²
potassium voltage-gated channel subfamily E regulatory subunit 3	<i>KCNE3</i>	0.73	4.64x10 ⁻²
G protein-coupled estrogen receptor 1	<i>GPER1</i>	0.60	4.67x10 ⁻²
mannose-P-dolichol utilization defect 1	<i>MPDU1</i>	1.48	4.67x10 ⁻²
heterogeneous nuclear ribonucleoprotein D	<i>HNRNPD</i>	1.55	4.68x10 ⁻²
BCL2 associated transcription factor 1	<i>BCLAF1</i>	1.69	4.73x10 ⁻²
ATP synthase F1 subunit epsilon pseudogene 2	<i>ATP5F1EP2</i>	0.74	4.75x10 ⁻²
zinc finger protein 626	<i>ZNF626</i>	0.52	4.78x10 ⁻²
heat shock protein 90 alpha family class A member 1	<i>HSP90AA1</i>	1.28	4.79x10 ⁻²
heat shock protein 90 beta family member 1	<i>HSP90B1</i>	1.52	4.79x10 ⁻²
EWS RNA binding protein 1	<i>EWSR1</i>	1.44	4.81x10 ⁻²
T cell receptor beta joining 1-6	<i>TRBJ1-6</i>	0.62	4.81x10 ⁻²
C-type lectin domain family 2 member B	<i>CLEC2B</i>	1.49	4.85x10 ⁻²
family with sequence similarity 46 member C	<i>FAM46C</i>	1.57	4.87x10 ⁻²
mitogen-activated protein kinase kinase kinase 3	<i>MAP3K3</i>	0.78	4.88x10 ⁻²
G protein-coupled receptor 150	<i>GPR150</i>	0.63	4.89x10 ⁻²
receptor transporter protein 4	<i>RTP4</i>	0.76	4.91x10 ⁻²
mitochondrial translational initiation factor 2	<i>MTIF2</i>	1.62	4.94x10 ⁻²
chromosome 15 open reading frame 40	<i>C15orf40</i>	0.68	4.98x10 ⁻²
zinc finger and BTB domain containing 12	<i>ZBTB12</i>	0.67	4.99x10 ⁻²

Biological Function	Genes involved (gene symbol)	FDR-adjusted P-value
Circadian Rhythm		
Circadian rhythm	<i>CREM, JUN, PER1, NAMPT</i>	1.5×10^{-2}
Circadian regulation of gene expression	<i>CREM, PER1, NAMPT</i>	2.0×10^{-2}
Metabolic Regulation		
Regulation of protein metabolic process	<i>CSRNPI, DDX3X, JUN, NFKBIA, PPP1R15A, RIPK2, TNFAIP3, UBE2D3, ZC3H12A</i>	6.3×10^{-3}
Negative regulation of cellular metabolic process	<i>CREM, DDX3X, ENC1, IER3, JUN, NFKBIA, PER1, SOCS3, TNFAIP3, UBE2D3, ZC3H12A, ZNF202, ZNF274</i>	3.6×10^{-3}
Regulation of primary metabolic processes	<i>ENC1, PILRB, IER3, ZNF274, JUN, UBE2D3, SOCS3, DDX3X, ETF1, NFKBIA, PER1, CCNL1, USP3, NAMPT, IL8, RIPK2, TNFAIP3, ZC3H12A, LPAR1, ZNF202</i>	2.7×10^{-3}
Stress Response		
Negative regulation of gene expression	<i>CREM, DDX3X, ENC1, UBE2D3, PER1, JUN, NFKBIA, PPP1R15A, TNFAIP3, ZNF202, ZC3H12A</i>	2.4×10^{-3}
Apoptotic process	<i>UBE2D3, JUN, PPP1R15A, DDX3X, NFKBIA, CSRNPI, TNFAIP3, RIPK2, ZC3H12A</i>	6.8×10^{-3}
Positive regulation of apoptotic process	<i>DCUN1D3, DDX3X, JUN, LPAR1, PMAIP1, RIPK2</i>	2.7×10^{-2}
Regulation of transcription from RNA Polymerase II promoter in response to stress	<i>JUN, PPP1R15A, UBE2D3</i>	2.0×10^{-2}
<i>Cellular response to stress*</i>	<i>IER3, UBE2D3, DDX3X, NFKBIA, IL8, TNFAIP3, RIPK2, USP3</i>	4.6×10^{-2}
Immune Inflammatory Response		
Response to Lipopolysaccharide (LPS)	<i>SOCS3, JUN, NFKBIA, IL8, TNFAIP3, RIPK2, ZC3H12A</i>	4.4×10^{-4}
Toll-like receptor 10 signaling pathway	<i>JUN, NFKBIA, RIPK2</i>	2.7×10^{-2}
Regulation of type I interferon production	<i>UBE2D3, NFKBIA, DDX3X, TNFAIP3, RIPK2</i>	1.3×10^{-3}
TRIF-dependent toll-like receptor signaling pathway	<i>UBE2D3, JUN, NFKBIA, RIPK2</i>	3.3×10^{-3}
Toll-like receptor 3 signaling pathway	<i>UBE2D3, JUN, NFKBIA, RIPK2</i>	3.8×10^{-3}
Toll-like receptor 4 signaling pathway	<i>UBE2D3, JUN, NFKBIA, RIPK2</i>	6.3×10^{-3}
Toll-like receptor 5 signaling pathway	<i>JUN, NFKBIA, RIPK2</i>	2.7×10^{-2}

Regulation of cytokine production	<i>DDX3X, NFKBIA, PER1, RIPK2, TNFAIP3, UBE2D3, ZC3H12A</i>	4.2×10^{-3}
Toll-like receptor 9 signaling pathway	<i>JUN, NFKBIA, RIPK2</i>	3.1×10^{-2}
MyD88-dependent toll-like receptor signaling pathway	<i>JUN, NFKBIA, RIPK2</i>	4.0×10^{-2}
Toll-like receptor 2 signaling pathway	<i>JUN, NFKBIA, RIPK2</i>	3.2×10^{-2}
Response to dsRNA	<i>NFKBIA, PMAIP1, RIPK2</i>	3.0×10^{-2}
<i>Innate immune response*</i>	<i>UBE2D3, SOCS3, JUN, NFKBIA, DDX3X, TNFAIP3, RIPK2</i>	1.5×10^{-2}
<i>Immune response*</i>	<i>UBE2D3, SOCS, JUN, DDX3X, NFKBIA, IL8, TNFAIP3, RIPK2</i>	1.6×10^{-2}
<i>Defense response*</i>	<i>PMAIP1, UBE2D3, SOCS3, JUN, DDX3X, NFKBIA, IL8, TNFAIP3</i>	2.2×10^{-2}
<i>Regulation of the inflammatory response*</i>	<i>IER3, SOCS3, PER1, TNFAIP3</i>	2.9×10^{-2}

Supplementary Table S3. Functional association networks of differentially expressed gene transcripts in the ME/CFS group. The table showed biological pathways indicated by Functional Network Analysis (FNA) to be enriched (False Discovery Rate-adjusted *P*-value <0.05) by the differentially expressed gene transcripts (*n*=33) in the ME/CFS cohort.

*Indicates biological pathways enriched after FNA of the increased gene transcripts (*n*=27).

Canonical Pathways	Genes Involved	P-value	Z-score	Overlap
Production of NO and ROS in macrophages	<i>JUN, PRKD3, PPP1CB, PPP2R1A, RHOQ, PRKCH, NFKBIA, MAP3K3, RELA</i>	1.8×10^{-5}	1	4.6% 9/194
LPS-stimulated MAPK signalling	<i>JUN, KRAS, PRKD3, PRKCH, NFKBIA, RELA</i>	5.3×10^{-5}	2.5	6.9% 6/87
NF-B activation by viruses	<i>KRAS, PRKD3, PRKCH, ITGB2, NFKBIA, RELA</i>	5.3×10^{-5}	1.6	6.9% 6/87
IL-8 signalling	<i>JUN, KRAS, PRKD3, RHOQ, ITGB2, PRKCH, IL8, RELA</i>	1.4×10^{-4}	2.1	4.1% 8/197
TNFR2 signalling	<i>JUN, TNFAIP3, NFKBIA, RELA</i>	7.5×10^{-5}	-	13.3% 4/30
PPAR signalling	<i>JUN, KRAS, HSP90B1, NFKBIA,</i>	8.7×10^{-5}	-2.5	6.3% 6/95

HSP90AA1, RELA

Supplementary Table S4. Canonical pathways identified by IPA analysis from altered gene expression of transcripts in the ME/CFS group. Canonical pathways identified from the gene transcript dataset ($P<0.05$), with the most highly significant enrichment scores (P -value) measuring the overlap of observed and predicted regulated gene sets, and z-scores assessing the match of observed and predicted regulation. Pathways with z-scores of >2 or <-2 are considered activated or inhibited, respectively. Overlap states the number (also expressed as a percentage) of matching changed gene transcripts in the dataset with the genes involved in each canonical pathway.

Regulator effect networks	Diseases and functions	Consistency score
FOXO1, Hdac, HGF, IL1B, IL6, JNK, NFKB (complex), PDGF BB	Oxidative stress and inflammation of the liver	13.9
CREB1, EGF, IL1B, JNK, PDGF BB, STAT3, TNF	Oxidative stress	11.6
EGF, IFNG, IL3, NFKB (complex), TNF, TNFSF11	Damage of nervous tissue	8.9

Supplementary Table S5. Regulator networks linked to ME/CFS. IPA identifies regulator effect networks based on the gene transcript dataset with a consistency score given for identified networks. The consistency score is based on the consistency of relationships within the identified network. A consistent relationship is one in which the direction of node activity/expression that is observed or predicted is consistent with the direction one would expect based on the findings from the Ingenuity Knowledge Base.